Election/Restriction

The Examiner has requested the election of one of the claimed ribozymes of claims 1, 11, 15 and 18. In response, applicants elect the ribozyme of claim 1 with traverse. However, applicants respectfully note that it is not exactly clear what precisely the Examiner has requested applicants to "elect", given applicants' understanding of the technology of the claimed invention. Applicants respectfully submit the following.

Based on the Examiner's reference to MPEP 2434, applicants believe that the Examiner essentially has considered that the claimed subject matter relates to a plurality of nucleotide sequences, noting that the policy of the Patent and Trademark Office is to limit the number of nucleotide sequences so claimed to not more than ten in a single application. Applicants respectfully disagree, and submit that the claims are not directed to a mere collection of nucleotide sequences, but rather, are directed to an enzyme having a certain structure defined by certain physical and chemical characteristics. These characteristics are succinctly defined in the claims to allow one of skill in the art to recognize the claimed enzyme. Via extensive experimental testing as described in the application, applicants have determined the central characteristics of the enzyme, which form the basis of the defining characteristics recited in the claims. As such, claims 1, 11, 14, 15 and 18 have been amended for clarity to more clearly reflect this point. Defining the enzyme in this way is no different that defining it in terms of any other physical or chemical characteristics which uniquely serve to define a product.

The Examiner has further noted that a search of the claimed subject matter presents an undue burden on the Patent and Trademark Office. Applicants respectfully disagree, as applicants believe that the Examiner's comments in this regard are based purely on a presumption of nucleotide sequence-based searching, which is not the case here. For example, claim 1 defines the structure of six features of the enzyme, as defined in parts (a) to (f). Collectively, these characteristics define the enzyme of claim 1 and may be used for searching. As such, the search does not entail a search of random nucleic acid sequences, but rather, involves searching in the field of nucleic acid enzymes

to ascertain the prior art in this field with respect to the characteristics recited in the claims which define the nucleic acid enzyme of the instant application.

Further, upon a brief review of issued US Patents, applicants respectfully submit that such a claim structure is frequently utilized and accepted under US practice. Consider, for example, the following:

Claim 2 of US Patent 6,433,154

> 2. A nucleic acid encoding a fusion protein, wherein the fusion protein comprises:
>
> a) an extracellular ligand-binding domain of human epidermal growth factor receptor, and
>
> b) an intracellular kinase domain of SLN1 capable of transferring a phosphate to YPD1 upon binding of a ligand to the extracellular ligand-binding domain of human epidermal growth factor receptor.

In this case, the nucleic acid is defined by encoding a protein comprising two particular domains.

Claim 1 of US Patent 6,329,178

> 1. A mutant DNA polymerase within the Pol I family of polymerases comprising a mutation in an active site of a naturally occurring DNA polymerase, wherein said active site comprises an amino acid sequence of DYSQIELR (SEQ ID NO: 2), said mutation comprises an alteration of an amino acid other than E in said sequence, and said mutant DNA polymerase possesses altered fidelity or altered catalytic activity in comparison with said naturally occurring DNA polymerase.

In this case, the mutant polymerase is defined by a short sequence in its active site and its activity, noting that with the exception of the "E" residue, all other residues in the active site are variable.

Numerous other similar examples exist. Applicants respectfully submit that they believe the scenario described by the Examiner and that envisioned by the cited passage MPEP 2434 is not applicable in this case, as the claimed subject matter relates to a

nucleic acid enzyme defined by very specific clearly recited characteristics, and not to a mere collection of nucleic acid sequences.

In light of the above, applicants respectfully request that the election requirement be withdrawn.

Claims 14 to 17 have been amended to correct a typographical error, to amend "claims" to correctly read "claim".

It is believed this responds to all of the Examiner's concerns, however if the Examiner has any further questions, he is invited to contact Joy Morrow at 613-232-2486. Further, If the Examiner does not consider that the application is in a form for allowance, an interview with the Examiner is respectfully requested.

Respectfully submitted,

August 30, 2002
~~September~~
Date

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APPENDIX: VERSION WITH MARKINGS TO SHOW CHANGES MADE

1. A nucleic acid enzyme capable of recognizing and cleaving a nucleic acid substrate at a cleavage site which when bound to the substrate comprises:

(a) a substrate binding portion base-paired to the 6 nucleotides 3' to the cleavage site of the substrate and which binding portion comprises [the sequence:

3'-UNNXNN-5'

wherein each

N is a nucleotide which may be the same or different, and

X is a nucleotide selected from the group consisting of T, U, A, G] a six nucleotide sequence wherein its 3'-most first position is a uracil nucleotide and its fourth position is a nucleotide other than a cytosine nucleotide;

(b) a region P3 comprising a double-stranded portion bound covalently at a bottom end to the remainder of the ribozyme and capped at a top end by a loop L3;

(c) a region P2 comprising a double-stranded portion bound covalently at a bottom end to the remainder of the ribozyme;

(d) a region P4 comprising a double-stranded portion bound covalently at a bottom end to the remainder of the ribozyme, wherein the first base-pair at the bottom end of P4 is a homopurine base-pair;

(e) a double-stranded region P1.1 formed by base-pairing two nucleotides located between the substrate binding portion and the P4 region, with two nucleotides in the L3 loop; and

(f) a single-stranded region, J4/2, covalently bound at one end to the bottom end of P2 and covalently bound at the

other end to the bottom end of P4.

11. The nucleic acid enzyme according to claim 1, wherein the double-stranded portion of the P4 region comprises [the sequence 5′-GCAUSG-3′ or 5′-GCAUSSG-3′, wherein S is G or C] a sequence selected from the group consisting of 5′-GCAUGG-3′, 5′-GCAUCG-3′, 5′-GCAUGGG-3′, 5′-GCAUCCG-3′, 5′-GCAUGCG-3′and 5′-GCAUCGG-3′.

14. The nucleic acid enzyme of claim[s] 1, wherein the substrate binding portion of the enzyme additionally comprises [the sequence 3'-UNNXNNN-5'] a seventh nucleotide attached to the 5′-most end of the six nucleotide sequence.

15. The nucleic acid enzyme of claim 14, wherein the [substrate binding portion of the enzyme comprises the sequences 3'-UNNANNN-5' or 3'-UNNGNNN-5'] nucleotide other than a cytosine nucleotide is a nucleotide selected from the group consisting of an adenine nucleotide and a guanine nucleotide.

16. The nucleic acid enzyme of claim[s] 1, wherein the enzyme is composed of ribonucleotides.

17. The nucleic acid enzyme of claim[s] 1, wherein the enzyme is composed of a mixture of ribonucleotides and deoxyribonucleotides.

18. A method for cleaving a nucleic acid substrate with a nucleic acid enzyme at a cleavage site comprising mixing the nucleic acid enzyme according to any one of claims 1 to 17 with the substrate, wherein

the substrate includes a 7 nucleotide sequence with at least 6 nucleotides 3′ to the cleavage site and at least 1 nucleotide 5′ to the cleavage site [and of formula:

5'-H′↓GNNHNN-3'

wherein each

N is a nucleotide which may be the same or different,

H is a nucleotide selected from the group consisting of A, U, C, and T,

↓ is the site of cleavage, and

H′ is a ribonucleotide selected from the group consisting of A, U, and C,] , wherein the first nucleotide 3′ to the cleavage site is a guanine nucleotide, the fourth nucleotide 3′ to the cleavage site is a nucleotide other that a guanine nucleotide, and the nucleotide 5′ to the cleavage site is a nucleotide other than a guanine nucleotide or a thymine nucleotide;

wherein

(i) the first nucleotide 3' to the cleavage site is capable of forming a wobble pair with the enzyme,

(ii) the second, third, fifth, and sixth nucleotides 3' to the cleavage site are capable of forming conventional Watson-Crick base pairs with the enzyme,

(iii) the fourth nucleotide 3' to the cleavage site is capable of forming a triplet with the enzyme comprising a non-conventional Watson-Crick base pair and a conventional Watson-Crick base pair, and

(iv) the ribonucleotide directly 5' to the cleavage site does not form a base pair with the enzyme.